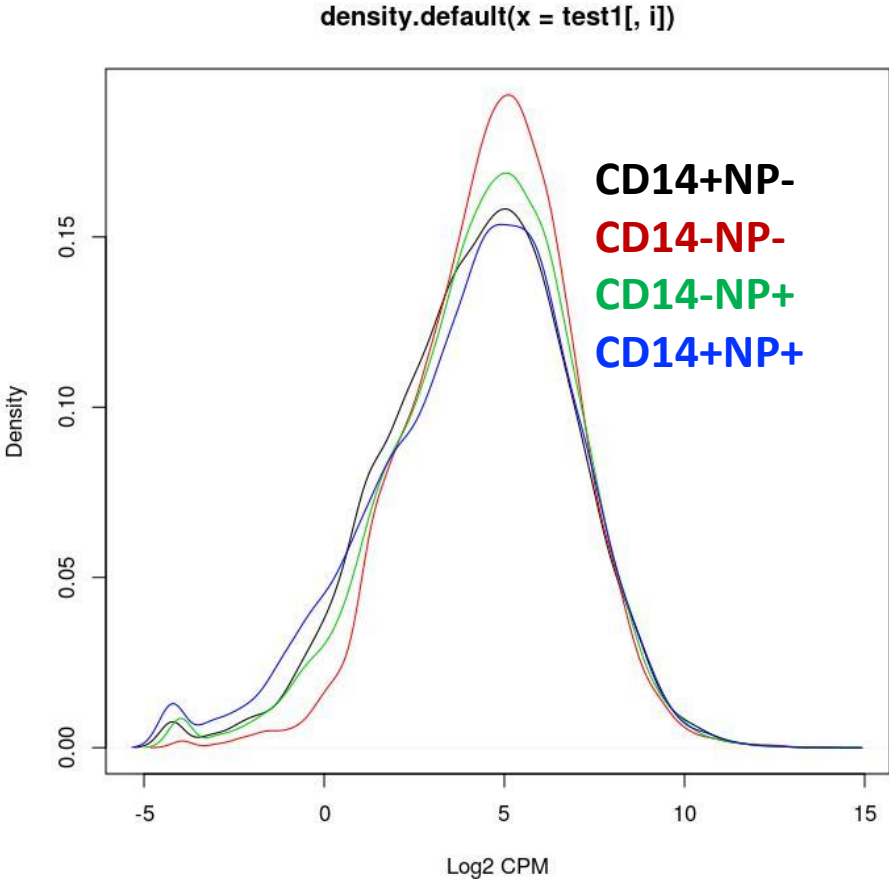
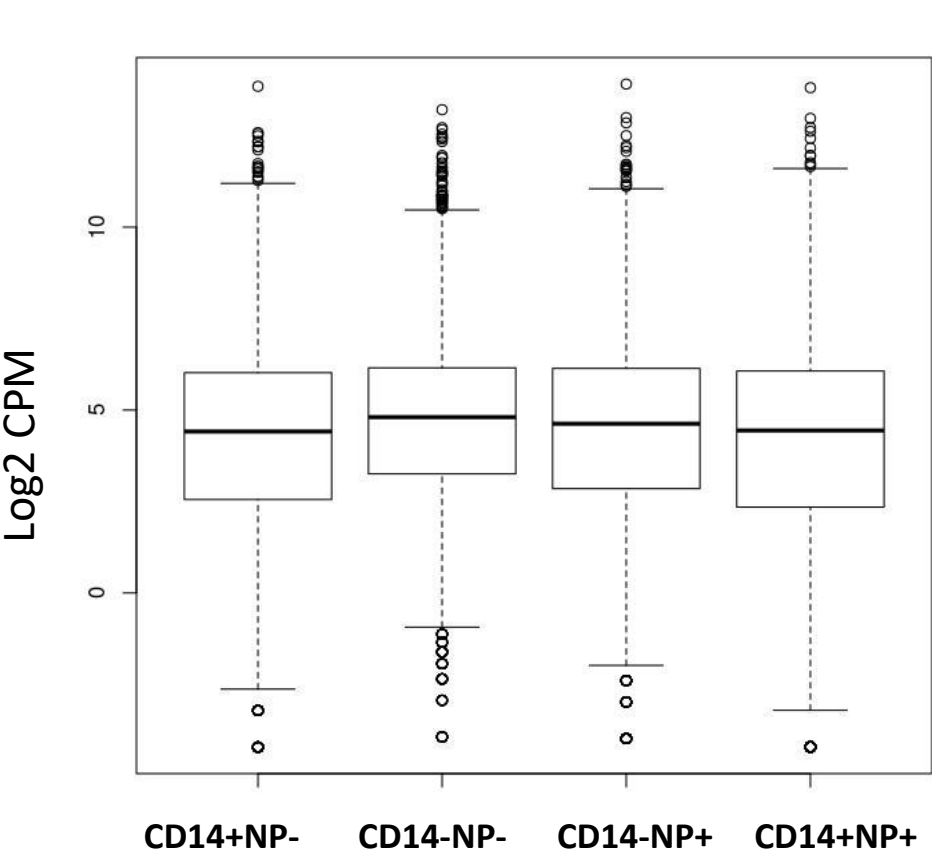


Supplementary Information S1: Sample QC for RNA-seq of sorted cells from WHV+ Woodchuck Experiment 3

	CD14+ NP-	CD14- NP-	CD14- NP+	CD14+ NP+
Total fragments sequenced :	36693444	27633516	26666663	32705550
Successfully assigned fragments :	20743633 (56.5%)	17433846 (63.1%)	17477941 (65.5%)	20057980 (61.3%)



The data was first normalized by counts-per-million (cpm) and then subjected to TMM (trimmed mean of M). TMM removes low count genes by cpm-cutoff to filter out noise. The values for cpm-cutoff were determined empirically for the minimum value required to achieve the best normalization among the samples (obtain a normal distribution among the samples). Furthermore, any genes with duplicated symbols are removed due to potential errors in the reference genome assembly. For this study, only protein-coding genes were used and the best cpm-cutoff is determined to be 2 and this value is examined by boxplots and density curves that shows a near-normal distribution.